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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/701,395ADATE: 05/08/2003
TIME: 14:48:25Input Set : A:\10817222.app
Output Set: N:\CRF4\05082003\I701395A.raw

3 <110> APPLICANT: CUNNINGHAM JR., FRANCIS X.
 4 SUN, ZAIREN
 6 <120> TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
 7 METHODS OF USE THEREOF
 9 <130> FILE REFERENCE: 108172-00022
 11 <140> CURRENT APPLICATION NUMBER: 09/701,395A
 12 <141> CURRENT FILING DATE: 2001-09-25
 14 <150> PRIOR APPLICATION NUMBER: 09/088,724
 15 <151> PRIOR FILING DATE: 1998-06-02
 17 <150> PRIOR APPLICATION NUMBER: 09/088,725
 18 <151> PRIOR FILING DATE: 1998-06-02
 20 <160> NUMBER OF SEQ ID NOS: 62
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1860
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Arabidopsis thaliana
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 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (109)..(1680)
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 37 Met Glu Cys
 38 1
 40 gtt ggg gct agg aat ttc gca gca atg gcg gtt tca aca ttt ccg tca 165
 41 Val Gly Ala Arg Asn Phe Ala Ala Met Ala Val Ser Thr Phe Pro Ser
 42 5 10 15
 44 tgg agt tgt cga agg aaa ttt cca gtg gtt aag aga tac agc tat agg 213
 45 Trp Ser Cys Arg Arg Lys Phe Pro Val Val Lys Arg Tyr Ser Tyr Arg
 46 .20 25 30 35
 48 aat att cgt ttc ggt ttg tgt agt gtc aga gct agc ggc ggc gga agt 261
 49 Asn Ile Arg Phe Gly Leu Cys Ser Val Arg Ala Ser Gly Gly Ser
 50 40 45 50
 52 tcc ggt agt gag agt tgt gta gcg gtg aga gaa gat ttc gct gac gaa 309
 53 Ser Gly Ser Glu Ser Cys Val Ala Val Arg Glu Asp Phe Ala Asp Glu
 54 55 60 65
 56 gaa gat ttt gtg aaa gct ggt ggt tct gag att cta ttt gtt caa atg 357
 57 Glu Asp Phe Val Lys Ala Gly Gly Ser Glu Ile Leu Phe Val Gln Met
 58 70 75 80
 60 cag cag aac aaa gat atg gat gaa cag tct aag ctt gtt gat aag ttg 405
 61 Gln Gln Asn Lys Asp Met Asp Glu Gln Ser Lys Leu Val Asp Lys Leu
 62 85 90 95

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64	cct	cct	ata	tca	att	ggt	gat	ggt	gct	ttg	gat	cat	gtg	gtt	att	ggt		453
65	Pro	Pro	Ile	Ser	Ile	Gly	Asp	Gly	Ala	Leu	Asp	His	Val	Val	Ile	Gly		
66	100				105					110						115		
68	tgt	ggt	cct	gct	ggt	tta	gcc	ttg	gct	gca	gaa	tca	gct	aag	ctt	gga		501
69	Cys	Gly	Pro	Ala	Gly	Leu	Ala	Leu	Ala	Ala	Glu	Ser	Ala	Lys	Leu	Gly		
70						120				125						130		
72	tta	aaa	gtt	gga	ctc	att	ggt	cca	gat	ctt	cct	ttt	act	aac	aat	tac		549
73	Leu	Lys	Val	Gly	Leu	Ile	Gly	Pro	Asp	Leu	Pro	Phe	Thr	Asn	Asn	Tyr		
74						135				140						145		
76	ggt	gtt	tgg	gaa	gat	gaa	ttc	aat	gat	ctt	ggg	ctg	caa	aaa	tgt	att		597
77	Gly	Val	Trp	Glu	Asp	Glu	Phe	Asn	Asp	Leu	Gly	Leu	Gln	Lys	Cys	Ile		
78						150				155						160		
80	gag	cat	gtt	tgg	aga	gag	act	att	gtg	tat	ctg	gat	gac	aag	cct			645
81	Glu	His	Val	Trp	Arg	Glu	Thr	Ile	Val	Tyr	Leu	Asp	Asp	Asp	Lys	Pro		
82						165				170						175		
84	att	acc	att	ggc	cgt	gct	tat	gga	aga	gtt	agt	cga	cgt	ttg	ctc	cat		693
85	Ile	Thr	Ile	Gly	Arg	Ala	Tyr	Gly	Arg	Val	Ser	Arg	Arg	Leu	Leu	His		
86						180				185						190		195
88	gag	gag	ctt	ttg	agg	agg	tgt	gtc	gag	tca	ggg	gtc	tcg	tac	ctt	agc		741
89	Glu	Glu	Leu	Leu	Arg	Arg	Cys	Val	Glu	Ser	Gly	Val	Ser	Tyr	Leu	Ser		
90						200				205						210		
92	tcg	aaa	gtt	gac	agc	ata	aca	gaa	gct	tct	gat	ggc	ctt	aga	ctt	gtt		789
93	Ser	Lys	Val	Asp	Ser	Ile	Thr	Glu	Ala	Ser	Asp	Gly	Leu	Arg	Leu	Val		
94						215				220						225		
96	gct	tgt	gac	gac	aat	aac	gtc	att	ccc	tgc	agg	ctt	gcc	act	gtt	gct		837
97	Ala	Cys	Asp	Asp	Asn	Asn	Val	Ile	Pro	Cys	Arg	Leu	Ala	Thr	Val	Ala		
98						230				235						240		
100	tct	gga	gca	gct	tcg	gga	aag	ctc	ttg	caa	tac	gaa	gtt	ggg	cct			885
101	Ser	Gly	Ala	Ala	Ser	Gly	Lys	Leu	Leu	Gln	Tyr	Glu	Val	Gly	Gly	Pro		
102						245				250						255		
104	aga	gtc	tgt	gtg	caa	act	gca	tac	ggc	gtg	gag	gtt	gag	gtg	gaa	aat		933
105	Arg	Val	Cys	Val	Gln	Thr	Ala	Tyr	Gly	Val	Glu	Val	Glu	Val	Glu	Asn		
106						260				265						270		275
108	agt	cca	tat	gat	cca	atg	gtt	ttc	atg	gat	tac	aga	gat	tat				981
109	Ser	Pro	Tyr	Asp	Pro	Asp	Gln	Met	Val	Phe	Met	Asp	Tyr	Arg	Asp	Tyr		
110						280				285						290		
112	act	aac	gag	aaa	gtt	cg	agc	tta	gaa	gct	gag	tat	cca	acg	ttt	ctg		1029
113	Thr	Asn	Glu	Lys	Val	Arg	Ser	Leu	Glu	Ala	Glu	Tyr	Pro	Thr	Phe	Leu		
114						295				300						305		
116	tac	gcc	atg	cct	atg	aca	aag	tca	aga	ctc	ttc	gag	gag	aca	tgt			1077
117	Tyr	Ala	Met	Pro	Met	Thr	Lys	Ser	Arg	Leu	Phe	Phe	Glu	Glu	Thr	Cys		
118						310				315						320		
120	ttg	gcc	tca	aaa	gat	gtc	atg	ccc	ttt	gat	ttg	cta	aaa	acg	aag	ctc		1125
121	Leu	Ala	Ser	Lys	Asp	Val	Met	Pro	Phe	Asp	Leu	Leu	Lys	Thr	Lys	Leu		
122						325				330						335		
124	atg	tta	aga	tta	gat	aca	ctc	gga	att	cga	att	cta	aag	act	tac	gaa		1173
125	Met	Leu	Arg	Leu	Asp	Thr	Leu	Gly	Ile	Arg	Ile	Leu	Lys	Thr	Tyr	Glu		
126						340				345						350		355
128	gag	gag	tgg	tcc	tat	atc	cca	gtt	ggt	tcc	ttg	cca	aac	acc	gaa			1221

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132	caa	aag	aat	ctc	gcc	ttt	ggt	gct	gcc	gct	agc	atg	gta	cat	ccc	gca
133	Gln	Lys	Asn	Leu	Ala	Phe	Gly	Ala	Ala	Ala	Ser	Met	Val	His	Pro	Ala
134									375		380					385
136	aca	ggc	tat	tca	gtt	gtg	aga	tct	ttg	tct	gaa	gct	cca	aaa	tat	gca
137	Thr	Gly	Tyr	Ser	Val	Val	Arg	Ser	Leu	Ser	Glu	Ala	Pro	Lys	Tyr	Ala
138									390		395					400
140	tca	gtc	atc	gca	gag	ata	cta	aga	gaa	gag	act	acc	aaa	cag	atc	aac
141	Ser	Val	Ile	Ala	Glu	Ile	Leu	Arg	Glu	Glu	Thr	Thr	Lys	Gln	Ile	Asn
142									405		410					415
144	agt	aat	att	tca	aga	caa	gct	tgg	gat	act	tta	tgg	cca	cca	gaa	agg
145	Ser	Asn	Ile	Ser	Arg	Gln	Ala	Trp	Asp	Thr	Leu	Trp	Pro	Pro	Glu	Arg
146									420		425					435
148	aaa	aga	cag	aga	gca	ttc	ttt	ctc	ttt	ggt	ctt	gca	ctc	ata	gtt	caa
149	Lys	Arg	Gln	Arg	Ala	Phe	Phe	Leu	Phe	Gly	Leu	Ala	Leu	Ile	Val	Gln
150									440		445					450
152	ttc	gat	acc	gaa	ggc	att	aga	agc	ttc	tgc	act	ttc	ttc	cgc	ctt	
153	Phe	Asp	Thr	Glu	Gly	Ile	Arg	Ser	Phe	Phe	Arg	Thr	Phe	Phe	Arg	Leu
154									455		460					465
156	cca	aaa	tgg	atg	tgg	caa	ggg	ttt	ctt	gga	tca	aca	tta	aca	tca	gga
157	Pro	Lys	Trp	Met	Trp	Gln	Gly	Phe	Leu	Gly	Ser	Thr	Leu	Thr	Ser	Gly
158									470		475					480
160	gat	ctc	gtt	ctc	ttt	gct	tta	tac	atg	ttc	gtc	att	tca	cca	aac	aat
161	Asp	Leu	Val	Leu	Phe	Ala	Leu	Tyr	Met	Phe	Val	Ile	Ser	Pro	Asn	Asn
162									485		490					495
164	ttg	aga	aaa	ggt	ctc	atc	aat	cat	ctc	atc	tct	gat	cca	acc	gga	gca
165	Leu	Arg	Lys	Gly	Leu	Ile	Asn	His	Leu	Ile	Ser	Asp	Pro	Thr	Gly	Ala
166									500		505					515
168	acc	atg	ata	aaa	acc	tat	ctc	aaa	gta	tgattttactt	atcaactctt					1700
169	Thr	Met	Ile	Lys	Thr	Tyr	Leu	Lys	Val							
170									520							
172	aggtttgtgt	atatatatgt	tgattttatct	gaataatcg	tcaaagaatg	gtatgtgggt										1760
174	tacttaggaag	ttggaaacaa	acatgtata	aatctaagga	gtgatcgaaa	tggagatgg										1820
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188	Phe	Pro	Ser	Trp	Ser	Cys	Arg	Arg	Lys	Phe	Pro	Val	Val	Lys	Arg	Tyr
189									20		25					30
191	Ser	Tyr	Arg	Asn	Ile	Arg	Phe	Gly	Leu	Cys	Ser	Val	Arg	Ala	Ser	Gly
192									35		40					45
194	Gly	Gly	Ser	Ser	Gly	Ser	Glu	Ser	Cys	Val	Ala	Val	Arg	Glu	Asp	Phe
195									50		55					60
197	Ala	Asp	Glu	Glu	Asp	Phe	Val	Lys	Ala	Gly	Gly	Ser	Glu	Ile	Leu	Phe

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203	Asp Lys Leu Pro Pro Ile Ser Ile Gly Asp Gly Ala Leu Asp His Val			
204	100	105	110	
206	Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Ala Glu Ser Ala			
207	115	120	125	
209	Lys Leu Gly Leu Lys Val Gly Leu Ile Gly Pro Asp Leu Pro Phe Thr			
210	130	135	140	
212	Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Asn Asp Leu Gly Leu Gln			
213	145	150	155	160
215	Lys Cys Ile Glu His Val Trp Arg Glu Thr Ile Val Tyr Leu Asp Asp			
216	165	170	175	
218	Asp Lys Pro Ile Thr Ile Gly Arg Ala Tyr Gly Arg Val Ser Arg Arg			
219	180	185	190	
221	Leu Leu His Glu Glu Leu Leu Arg Arg Cys Val Glu Ser Gly Val Ser			
222	195	200	205	
224	Tyr Leu Ser Ser Lys Val Asp Ser Ile Thr Glu Ala Ser Asp Gly Leu			
225	210	215	220	
227	Arg Leu Val Ala Cys Asp Asp Asn Asn Val Ile Pro Cys Arg Leu Ala			
228	225	230	235	240
230	Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr Glu Val			
231	245	250	255	
233	Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Val Glu Val Glu			
234	260	265	270	
236	Val Glu Asn Ser Pro Tyr Asp Pro Asp Gln Met Val Phe Met Asp Tyr			
237	275	280	285	
239	Arg Asp Tyr Thr Asn Glu Lys Val Arg Ser Leu Glu Ala Glu Tyr Pro			
240	290	295	300	
242	Thr Phe Leu Tyr Ala Met Pro Met Thr Lys Ser Arg Leu Phe Phe Glu			
243	305	310	315	320
245	Glu Thr Cys Leu Ala Ser Lys Asp Val Met Pro Phe Asp Leu Leu Lys			
246	325	330	335	
248	Thr Lys Leu Met Leu Arg Leu Asp Thr Leu Gly Ile Arg Ile Leu Lys			
249	340	345	350	
251	Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser Leu Pro			
252	355	360	365	
254	Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser Met Val			
255	370	375	380	
257	His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu Ala Pro			
258	385	390	395	400
260	Lys Tyr Ala Ser Val Ile Ala Glu Ile Leu Arg Glu Glu Thr Thr Lys			
261	405	410	415	
263	Gln Ile Asn Ser Asn Ile Ser Arg Gln Ala Trp Asp Thr Leu Trp Pro			
264	420	425	430	
266	Pro Glu Arg Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu			
267	435	440	445	
269	Ile Val Gln Phe Asp Thr Glu Gly Ile Arg Ser Phe Phe Arg Thr Phe			
270	450	455	460	

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272 Phe Arg Leu Pro Lys Trp Met Trp Gln Gly Phe Leu Gly Ser Thr Leu
273 465 470 475 480
275 Thr Ser Gly Asp Leu Val Leu Phe Ala Leu Tyr Met Phe Val Ile Ser
276 485 490 495
278 Pro Asn Asn Leu Arg Lys Gly Leu Ile Asn His Leu Ile Ser Asp Pro
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282 515 520
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287 <211> LENGTH: 956
288 <212> TYPE: DNA
289 <213> ORGANISM: Arabidopsis thaliana
291 <400> SEQUENCE: 3
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294 agaattctcc gattgagaac gatgagagac cggagagcac gagctccaca aacgctata 180
295 acgctgagta tctggcgttg cggttggcgg agaaatttgg aaggaagaaa tcggagagg 240
296 ccacttatct aatcgctgct atgttgcga gctttggat cacttctatg gctgttatgg 300
297 ctgtttacta cagattctct tggcaaattgg agggaggtga gatctcaatg ttgaaatgt 360
298 ttggtagtatt tgctctctct gttggtgctg ctgttggat ggaattctgg gcaagatggg 420
299 ctcatagagc tctgtggcac gcttctctat ggaatatgca tgagtcaatc cacaacc 480
300 gagaaggacc gtttgagcta aacgatgtt ttgcataatg gaacgctggc ccagcgattg 540
301 gtctcccttc ttatggattc ttcataaaag gactcggtcc tggctctgc tttggcgcc 600
302 gtttaggcat aacgggtttt ggaatcgctt acatgtttt ccacgatgtt ctcgtgcaca 660
303 agcgcccccc ttaggtccc atcgccgacg tcccttacct ccgaaaggcc gccgccgtc 720
304 accagctaca tcacacagac aagttcaatg gtgtaccata tggactgtt cttggacc 780
305 aggaatttggg agaagttggg ggaaatgaag agtagataa ggagattagt cggagaatca 840
306 aatcatacaa aaaggccctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt 900
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311 <211> LENGTH: 294
312 <212> TYPE: PRT
313 <213> ORGANISM: Arabidopsis thaliana
315 <400> SEQUENCE: 4
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317 1 5 10 15
319 Leu Ser Gly Phe Ser Pro Ser Leu Arg Phe Lys Arg Phe Ser Val Cys
320 20 25 30
322 Tyr Val Val Glu Glu Arg Arg Gln Asn Ser Pro Ile Glu Asn Asp Glu
323 35 40 45
325 Arg Pro Glu Ser Thr Ser Ser Thr Asn Ala Ile Asp Ala Glu Tyr Leu
326 50 55 60
328 Ala Leu Arg Leu Ala Glu Lys Leu Glu Arg Lys Lys Ser Glu Arg Ser
329 65 70 75 80
331 Thr Tyr Leu Ile Ala Ala Met Leu Ser Ser Phe Gly Ile Thr Ser Met
332 85 90 95
334 Ala Val Met Ala Val Tyr Tyr Arg Phe Ser Trp Gln Met Glu Gly Gly
335 100 105 110
337 Glu Ile Ser Met Leu Glu Met Phe Gly Thr Phe Ala Leu Ser Val Gly

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/08/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 366,367,368,369,370,371,372,373,374,375,376,377,378,379,380
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Seq#:21; Xaa Pos. 321
Seq#:24; N Pos. 7,8,9,10,11,1020,1180,1181,1330
Seq#:25; Xaa Pos. 336
Seq#:26; Xaa Pos. 491
Seq#:34; N Pos. 565,569
Seq#:48; Xaa Pos. 336

VERIFICATION SUMMARY**PATENT APPLICATION: US/09/701,395A****DATE: 05/08/2003****TIME: 14:48:26****Input Set : A:\10817222.app****Output Set: N:\CRF4\05082003\I701395A.raw**

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M:341 Repeated in SeqNo=13
L:1641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
M:341 Repeated in SeqNo=20
L:1809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:320
L:2024 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24
L:2120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:320
L:2238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:480
L:2527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:540
L:3366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:320